SEQUENCE LISTING

<110> Ress-Loeschke, Marion
Friedrich, Thomas
Hauer, Bernhard

<120> A process for preparing chiral carboxylic acids from nitriles using a nitrilase or microorganisms which comprise a gene for the nitrilase

<130> 49462
<140> US 09/806,876
<141> 2001-05-21

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<151> 1998-10-19

<160> 9

<170> WordPerfect version 6.1

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<213> Alcaligenes faecalis

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ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct        96
Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
            20                  25                  30

cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc       144
Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
        35                  40                  45

tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg       192
Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
    50                  55                  60

tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac       240
Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
65                  70                  75                  80
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agt gca gag ttt caa cgc att gcc cag gcc gca cgg acc ttg ggt att       288
Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
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ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg       336
Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
            100                 105                 110

ggc caa tgc ctg atc gac gac aag ggc gag atg ctg tgg tcg cgt cgc       384
Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
        115                 120                 125

aaa ctc aaa ccc acg cat gta gag cgc acc gta ttt ggt gaa ggt tat       432
Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
    130                 135                 140

gcc cgt gat ctg att gtg tcc gac aca gaa ctg gga cgc gtc ggt gct       480
Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
145                 150                 155                 160

cta tgc tgc tgg gag cat ttg tcg ccc ttg agc aag tac gcg ctg tac       528
Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
                165                 170                 175

tcc cag cat gaa gcc att cac att gct gcc tgg ccg tcg ttt tcg cta       576
Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
            180                 185                 190

tac agc gaa cag gcc cac gcc ctc agt gcc aag gtg aac atg gct gcc       624
Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
        195                 200                 205

tcg caa atc tat tcg gtt gaa ggc cag tgc ttt acc atc gcc gcc agc       672
Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
    210                 215                 220

agt gtg gtc acc caa gag acg cta gac atg ctg gaa gtg ggt gaa cac       720
Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His
225                 230                 235                 240

aac gcc ccc ttg ctg aaa gtg ggc ggc ggc agt tcc atg att ttt gcg       768
Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala
                245                 250                 255

ccg gac gga cgc aca ctg gct ccc tac ctg cct cac gat gcc gag ggc       816
Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly
            260                 265                 270

ttg atc att gcc gat ctg aat atg gag gag att gcc ttc gcc aaa gcg       864
Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala
        275                 280                 285
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Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu
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gtg ctg gac ttg ggg cac cga gac ccc atg act cgg gtg cac tcc aaa 960
Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys
305 310 315 320

agc gtg acc agg gaa gag gct ccc gag caa ggt gtg caa agc aag att 1008
Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile
325 330 335

gcc tca gtc gct atc agc cat cca cag gac tcg gac aca ctg cta gtg 1056
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Gln Glu Pro Ser
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Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
20 25 30

Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
35 40 45

Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
50 55 60

Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
65 70 75 80

Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
85 90 95

Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
100 105 110

Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
115 120 125

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Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
    130                 135                 140

Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
145                 150                 155                 160

Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
                165                 170                 175

Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
            180                 185                 190

Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
        195                 200                 205

Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
    210                 215                 220

Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His
225                 230                 235                 240

Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala
                245                 250                 255

Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly
            260                 265                 270

Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala
        275                 280                 285

Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu
    290                 295                 300

Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys
305                 310                 315                 320

Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile
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Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val
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Gln Glu Pro Ser
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<400> 3

Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser
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Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
20 25 30

Arg Gln Ala Arg Asp Glu Gly
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<213> Alcaligenes faecalis

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Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile Ala Ser Val Ala
1 5 10 15

Ile Ser His Pro Gln
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Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys
1 5 10

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atgcagacna gnaaratcgt scg 23

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ttaatcatat gcagacaaga aaaatcgtcc g 31

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aaggatcctc aagacggctc ttgcactagc ag 32--